

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 06:03:39 ; Search time 3394 Seconds
(Without Alignments)
10964.527 Million cell updates/sec

Title: US-09-939-537-32
Perfect score: 768
Sequence: 1 GCTAGAGAGAGCCCAATCTT.....GGGCTCTGAGCAGCAGATCC 768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	768	100.0	768	6 AR067945	AR067945 Sequence
2	768	100.0	768	6 AR166804	AR166804 Sequence
3	768	100.0	768	6 AR560090	AR560090 Sequence
4	744.6	97.0	3134	9 BC019046	BC019046 Homo sapi
5	738.2	96.1	3075	6 CQ851090	CQ851090 Sequence
6	738.2	96.1	3075	9 AK128301	AK128301 Homo sapi
7	701	91.3	3183	6 CQ851340	CQ851340 Sequence
8	701	91.3	3183	9 AK128579	AK128579 Homo sapi
9	701	91.3	4240	9 AK090464	AK090464 Homo sapi
10	695.2	90.5	7427	6 CQ768745	CQ768745 Sequence
11	695.2	90.5	7427	6 CQ768742	CQ768742 Sequence
12	694.4	90.4	1413	6 AX556949	AX556949 Sequence
13	694.4	90.4	1413	6 AX709548	AX709548 Sequence
14	694.4	90.4	1428	6 AR031186	AR031186 Sequence
15	694.4	90.4	1428	6 AR042591	AR042591 Sequence
16	694.4	90.4	1428	6 AR052284	AR052284 Sequence
17	694.4	90.4	1428	6 AR076262	AR076262 Sequence
18	694.4	90.4	1428	6 AR300619	AR300619 Sequence
19	694.4	90.4	1431	6 AR108863	AR108863 Sequence

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22	694.4	90.4	1431	6 AR265201	AR265201 Sequence
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24	694.4	90.4	1431	6 AR488223	AR488223 Sequence
25	694.4	90.4	1431	6 BD063035	BD063035 Identif
26	694.4	90.4	1431	6 BD063039	BD063039 Identif
27	694.4	90.4	1437	6 AR108865	AR108865 Sequence
28	694.4	90.4	1437	6 AR265199	AR265199 Sequence
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31	694.4	90.4	8540	6 BD004713	BD004713 Chimeric
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33	694.4	90.4	9209	6 AR015961	AR015961 Sequence
34	694.4	90.4	9209	6 AR060920	AR060920 Sequence
35	694.4	90.4	9209	6 AR211052	AR211052 Sequence
36	694.4	90.4	9209	6 AR454341	AR454341 Sequence
37	694.4	90.4	9209	6 AX032414	AX032414 Chimeric
38	694.4	90.4	9209	6 BD004714	BD004714 Chimeric
39	694.4	90.4	18986	6 AR051652	AR051652 Sequence
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42	693.8	90.3	1367	6 AX039182	AX039182 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR067945 768 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5851828.
ACCESSION AR067945
VERSION AR067945.1 GI:5999167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 768)
AUTHORS Seed, B., Banapur, B., Romeo, C. and Kolanus, W.
TITLE Targeted cytolysis of HIV-infected cells by chimeric CD4 receptor-bearing cells
JOURNAL Patent: US 5851828-A 32 22-DEC-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 768; DB 6; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCTAGAGAGAGCCCAATCTTGTGACAACTCACATGCGCCGACCACTGA 60
QY 1 ACTCTGTGGGGGACGTCAGTCTTCTTCCGCAAAACCAAGACACCTGAT 120
DB 1 ACTCTGTGGGGGACGTCAGTCTTCTTCCGCAAAACCAAGACACCTGAT 120
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DB 181 CAACTTCACTGTATGCTGACGCGCTGTGAGGATTAATGCCAAGCGGGGA 240
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Db 241 GGAGGAGTCAACAGACGTTACCGGCTGTGAGGCTCTCTCAACCGTCTGACGAGACTG 300
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Qy 421 ATCCGGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480
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Db 601 CAAGAGAGGTGGCAGCAGGAGGAGAAAGTCTTCTCAATGCTCCGTGATGAGGCTCTGCA 660
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Db 661 CAACCACTACACGCAAGAAAGCTCTCCCTGTCTCCGGGCTGCAACTGAGACCTG 720
Qy 721 TGCTGAGGCCCAAGAGCGGGAGCTGGAAGGCTCTGAGCAAGCATCC 768
Db 721 TGCTGAGGCCCAAGAGCGGGAGCTGGAAGGCTCTGAGCAAGCATCC 768

RESULT 2
ARI66804 768 bp DNA linear PAT 17-OCT-2001
LOCUS ARI66804
DEFINITION Sequence 32 from patent US 6284240.
ACCESSION ARI66804
VERSION ARI66804.1 GI:16243146
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLE 1 (bases 1 to 768)
JOURNAL Seed, B., Banapour, B., Romeo, C. and Kolanus, W.
FEATURES Targeted cytolysis of HIV-infected cells by chimeric CD4
Patent: US 6284240-A 32 04-SEP-2001;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 768; DB 6; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTAGCAGAGCCCAATCTTGTGACAAACTCAACATGCGCCAGCAGCACTGGA 60
Db 1 GGTAGCAGAGCCCAATCTTGTGACAAACTCAACATGCGCCAGCAGCACTGGA 60
Qy 61 ACTCTGGGGGAGCCGTCACTCTTCTTCTTCCCAAAACCAAGACACCTCATGAT 120
Db 61 ACTCTGGGGGAGCCGTCACTCTTCTTCTTCCCAAAACCAAGACACCTCATGAT 120
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Db 301 GGTGATGGCAAGAGTCAAGTGAAGTCTTCCAAACAAGCCCTCCAGGCCCCATGCA 360
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Qy 421 ATCCGGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGCTCAAGGCTTTCTA 480
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Qy 721 TGCTGAGGCCCAAGAGCGGGAGCTGGAAGGCTCTGAGCAAGCATCC 768
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RESULT 3
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LOCUS ARS60090
DEFINITION Sequence 32 from patent US 6753162.
ACCESSION ARS60090
VERSION ARS60090.1 GI:53970430
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLE 1 (bases 1 to 768)
JOURNAL Seed, B., Banapour, B., Romeo, C. and Kolanus, W.
FEATURES Targeted cytolysis of HIV-infected cells by chimeric CD4
Patent: US 6753162-A 32 22-JUN-2004;
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 768; DB 6; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTAGCAGAGCCCAATCTTGTGACAAACTCAACATGCGCCAGCAGCACTGGA 60
Db 1 GGTAGCAGAGCCCAATCTTGTGACAAACTCAACATGCGCCAGCAGCACTGGA 60
Qy 61 ACTCTGGGGGAGCCGTCACTCTTCTTCTTCCCAAAACCAAGACACCTCATGAT 120
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QY 121 CTCCTCCGAGCCCTGAGGTCAATGCGGTGTTGTTGAGAGTGGACGAGAACCCCTGAGGT 180
DB 121 CTCCTCCGAGCCCTGAGGTCAATGCGGTGTTGTTGAGAGTGGACGAGAACCCCTGAGGT 180
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DB 301 GGTGAATGGCAAGAGTACAAAGTGCATAGTCTCAACAAAGCCCTCCAGCCCATCGA 360
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RESULT 4
LOCUS BC019046 3134 bp mRNA linear PRI 06-OCT-2003
DEFINITION Homo sapiens cDNA clone MGC:20691 IMAGE:4766140, complete cds.
ACCESSION BC019046
VERSION BC019046.2 GI:33879071
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bikarvoda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3134)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marais, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Abramson, R.D., Muliyil, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.D., Hult, K.S.W., Villalón, D.R., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helt, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

TITLE
JOURNAL
MEDLINE
PUBMED
22388257
12477932
2 (bases 1 to 3134)
Strausberg, R.
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:17512135.
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Akhter, N., Aylee, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granille, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Latic, P., Legaspi, R., Maduro, O.L., Masello, C., Maskeri, B., Masrini, S.D., McElroy, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
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Location/Qualifiers
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922. 1140
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Query Match	97.0%	Score 744.6	DB 9	Length 3134
Best Local Similarity	98.8%	Pred. No. 3.4e-15		
Matches 750; Conservative	0	Mismatches 9	Indels 0	Gaps 0

[illegible]

RESULT 5				
CO851090	CO851090	3075 bp	DNA	linear
LOCUS				
DEFINITION	Sequence 1559 from Patent EP1447413.			
ACCESSION	CO851090			
VERSION	CO851090.1	GI:51509302		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

REFERENCE	1
AUTHORS	Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T., Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.
TITLE	Full-length human CDNA
JOURNAL	Patent: EP 1447413-A 1559 18-AUG-2004;
FEATURES	Research Association for Biotechnology (JP)
source	Location/Qualifiers 1. .3075

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/db_xref="taxon:9606"

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Query Match	96.1%	Score 738.2;	DB 6;	Length 3075;
Best Local Similarity	98.3%;	Pred. No. 5.9e-134;		
Matches 746; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0

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QY	544 GCTTCCCTGCTGAGTCTCGACGAGCTCTTCTTCTCTTACAGCAAGCTCAACGTTGACAA	603
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QY	724 TGAAGCCCAAGACGGGGAGCTGAGCGGGCTGTGAGAGAC	782
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RESULT 6			
AK128301			
LOCUS	AK128301	3075 bp	mRNA linear PRI 19-FEB-2004

DEFINITION Homo sapiens cDNA FLJ46441 fis, clone THYMJ3016518, highly similar to Ig gamma-1 chain C region.

ACCESSION AK128301

VERSION AK128301.1 GI:34535606

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 2 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukumura, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Oka, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Nagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and Isogai, T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3075)

REFERENCE 1 Isogai, T. and Yamamoto, J.

AUTHORS Direct Submission

TITLE Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamata, Kisarazu, Chiba 292-0818, Japan

JOURNAL (E-mail:genominfo@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan Construction: Heli Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES

source

1. .3075

Location/Qualifiers

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38.1657

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ORIGIN

Query Match 96.1%; Score 738.2; DB 9; Length 3075;

Best Local Similarity 98.3%; Pred. No. 5.9e-134;

Matches 746; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 124 CCGGACCCCTGAGTCAATGCGTGTGTGTGACGTGAGCCAGAAAGCCTGAGTCA 183

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Db 928 GTTCAACTGAGTCACTGAGACGGCTGTGAGGTGCATTAATGCCAAGACAAAGCCGGGAGGA 987

Qy 244 GCAGTCAACAGACGTCACGGGTGTGTCAGCGGCTCCACCGTCTGTGACACAGGACTGGCT 303

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Qy 304 GAATGCAAGAGTCAAGTCAAGGCTTCCAAACAAGCCCTCCAGCCCTCCAGAGAA 363

Db 1048 GAATGCAAGAGTCAAGTCAAGGCTTCCAAACAAGCCCTCCAGCCCTCCAGAGAA 1107

Qy 364 AACCATCTCCAAAGCCAAAGGAGGAGCCCGAGAAACACAGGTGACACCTGCCCCATC 423

Db 1108 AACCATCTCCAAAGCCAAAGGAGGAGCCCGAGAAACACAGGTGACACCTGCCCCATC 1167

Qy 424 CCGGATGAGTCAACCAAGAACAGGTCAGCTGACCTGACCTGCTGCTGCTGATCC 483

Db 1168 CCGGATGAGTCAACCAAGAACAGGTCAGCTGACCTGACCTGCTGCTGCTGATCC 1227

Qy 484 CAGCAGATCGCCGTGAGTGGAGAGCAATGGGACCCGAGAACCAATCAAGACAC 543

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Qy 544 GCCTCCGTCGTGAGTCCGACGCGCTCTTCTTCTTCTTACAGAGTCACTGTGACAA 603

Db 1288 GCCTCCGTCGTGAGTCCGACGCGCTCTTCTTCTTCTTACAGAGTCACTGTGACAA 1347

Qy 604 GAGCAGTGGACAGAGGAGAAAGCTTTCATGCTCCGTGATGATGATGAGGCTGCAAA 663

Db 1348 GAGCAGTGGACAGAGGAGAAAGCTTTCATGCTCCGTGATGATGATGAGGCTGCAAA 1407

Qy 664 CCACTACAGCAGAAAGCTCTCCGTGCTCCGAGCTGCAACTGACAGACCTGTGC 723

Db 1408 CCACTACAGCAGAAAGCTCTCCGTGCTCCGAGCTGCAACTGACAGACCTGTGC 1467

Qy 724 TGAAGCCCAAGAGCGGAGAGTGGACGGGCTTGGAGCAC 762

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RESULT 7

Q0851340

LOCUS CQ851340 3183 bp DNA linear PAT 23-AUG-2004

DEFINITION Sequence 1809 from Patent EP1447413.

ACCESSION CQ851340

VERSION CQ851340.1 GI:51509552

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T., Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.

TITLE Full-length human cDNA

JOURNAL Patent: EP 1447413-A 1809 18-AUG-2004;

Research Association for Biotechnology (JP)

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 91.3%; Score 701; DB 6; Length 3183;

Best Local Similarity 95.4%; Pred. No. 1.1e-126;

Matches 722; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 926 TGGGAGAGACCGTCAGTCTTCTCTTCCCGCCAAAACCAAGATACCTTATGATTTCC 985
QY 126 GGAACCCCTGAGGTACATGCGTGTGTGTGACGTGACACGAAAGACCTGAGGTCAAGT 185
DB 986 GGAACCCCTGAGGTACATGCGTGTGTGTGACGTGACACGAAAGACCTGAGGTCAAGT 1045
QY 186 TCAACTGTGACGTGACGCGGTGTGACGATTAATGCAAGACCAAGACCGCGGAGAGAC 245
DB 1046 TCAAGTGTGACGTGACGCGGTGTGACGATTAATGCAAGACCAAGACCGCGGAGAGAC 1105
QY 246 AGTACAAAGACGATGACGCGGTGTGACGATGACGATGACGATGACGATGACGATGAC 305
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QY 426 GGGATGAGTGTGACCAAGACGATGACGATGACGATGACGATGACGATGACGATGAC 485
DB 1286 GGGATGAGTGTGACCAAGACGATGACGATGACGATGACGATGACGATGACGATGAC 1345
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DB 1346 GGGATGAGTGTGACCAAGACGATGACGATGACGATGACGATGACGATGACGATGAC 1405
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DB 1406 CTTCCGCTGTGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 1465
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DB 1466 GCGAGTGTGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 1525
QY 666 ACTACAGCAGAGAGAGGCTCTCCCTGCTCCGCGGCGTGAACCTGACGATGAC 725
DB 1526 GCTTACAGCAGAGAGAGGCTCTCCCTGCTCCGCGGCGTGAACCTGACGATGAC 1585
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RESULT 8
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LOCUS Homo sapiens cDNA FLJ46738 fis, clone TRACH3020930, highly similar
DEFINITION to IG gamma-1 chain C region.
ACCESSION AKI28579
VERSION AKI28579.1 GI:34536019
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoaka,S.,
Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Horiuta,T., Watanabe,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshina,A.,
Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K.,

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TITLE Masuo,Y., Nagai,K. and Isogai,T.
JOURNAL NEDO human cDNA sequencing project
REFERENCE 2 (bases 1 to 3183)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submision
JOURNAL Submitted (15-JUN-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: Reverse Proteomics Research Institute, HRI and
RAB.

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Query Match 91.3%; Score 701; DB 9; Length 3183;
Best Local Similarity 95.4%; Pred. No. 1.1e-126;
Matches 722; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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RESULT 10
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LOCUS CQ768745
DEFINITION Sequence 13 from Patent WO2004006962.
ACCESSION CQ768745
VERSION CQ768745.1 GI:45111935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS bJ Rn,S.R., Nicolaisen,E.M. and Steenstrup,T.D.
TITLE A tissue factor binding immunocoujugate comprising factor vlla
JOURNAL Patient: WO 2004006962-A 13 22-JAN-2004;
NOVO NORDISK A/S (DK)
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Best Local Similarity 98.2%; Pred. No. 1.3e-125;
Matches 703; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 665 CACTTCAAGCAGAGAGGCTCTCCCTGTCTCGGAGGTGCAACTGACGAGACCTG 720
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LOCUS CQ768742
DEFINITION Sequence 10 from Patent WO2004006962.
ACCESSION CQ768742
VERSION CQ768742.1 GI:45111927
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS bJ Rn,S.R., Nicolaisen,E.M. and Steenstrup,T.D.
TITLE A tissue factor binding immunocoujugate comprising factor vlla
JOURNAL Patient: WO 2004006962-A 10 22-JAN-2004;
NOVO NORDISK A/S (DK)
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source Location/Qualifiers
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Best Local Similarity 98.2%; Pred. No. 1.3e-125;
Matches 703; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 485 AGCGACATCGCGGTGAGTGGAGAGCAATGGGACCGGAGAACATTAACAAGACAG 544
DB 1895 AGCGACATCGCGGTGAGTGGAGAGCAATGGGACCGGAGAACATTAACAAGACAG 1954
QY 545 CTTCCCGTGTGAGTCCGACCGGCTCTTCTTCTTCAAGCAAGTCAAGTGAACAG 604
DB 1955 CTTCCCGTGTGAGTCCGACCGGCTCTTCTTCTTCAAGCAAGTCAAGTGAACAG 2014
QY 605 AGCAGGTGAGCAGAGGAGAAAGTCTTCAAGTCTCGGTGAGTGAAGGCTTGAACAG 664
DB 2015 AGCAGGTGAGCAGAGGAGAAAGTCTTCAAGTCTCGGTGAGTGAAGGCTTGAACAG 2074
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QY 665 CACTACACGAGAAAGCCCTCTCCCTGTCTCCGGGGCTGCACATGACAGACCTG 720
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RESULT 12
AX556949 1413 bp DNA linear PAT 27-NOV-2002
LOCUS Sequence 4 from Patent WO02060955.
DEFINITION AX556949
ACCESSION AX556949.1 GI:25900012
VERSION
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.

REFERENCE
1 Brajlawsky, G.R., Hanna, N. and Chinn, P.
AUTHORS Modified antibodies and methods of use
TITLE Patent: WO 02060955-A 4 08-AUG-2002;
JOURNAL Idex Pharmaceuticals Corporation (US)
FEATURES
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/note="Humanized C2B8 Heavy Chain Sequence"

ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1413;
Best Local Similarity 99.9%; Pred. No. 2.3e-125;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGCCAGACCTGAAT 63
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QY 64 CCGGGGGGAGCGTCAGTCTTCTCCCTCCCGCAAAACCAAGAGACCTCATGATCTC 123
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QY 124 CCGGACCCCTGAGGTCAATGCTGTGTGACGTGAGCCAGAGACCTTGAGGTCAA 183
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QY 184 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGCAATATGCCAAGCAAAAGCCGCGGAGGA 243
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QY 544 GCCTCCCGTGTGAGTCTCGAGCGGCTCTTCTTCTTACAGACGTTCAACGTTGAGCAA 603
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QY 604 GAGCAGTGGCAGCAGAGGAGACGTCTTCTCATGCTCCGTGATGACATGAGCTTCGACAA 663
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QY 664 CCACTACAGGCAGAGAGGCTTCTCCTGTCTCGGG 639
Db 1371 CCACTACAGGCAGAGAGGCTTCTCCTGTCTCGGG 1406

RESULT 13
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LOCUS Sequence 4 from Patent WO02096948.
DEFINITION AX709548
ACCESSION AX709548
VERSION AX709548.1 GI:29564973
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Brajlawsky, G.R., Hanna, N., Chinn, P. and Hariharan, K.
AUTHORS Engineered trivalent antibodies and methods of use
TITLE Patent: WO 02096948-A 4 05-DEC-2002;
JOURNAL Idex Pharmaceuticals Corporation (US)
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ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1413;
Best Local Similarity 99.9%; Pred. No. 2.3e-125;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGCCAGACCTGAAT 63
Db 711 AGCAGAGCCCAATCTTGTGACAAACTCAACATGCCCGCCAGACCTGAAT 770

QY 64 CCGGGGGGAGCGTCAGTCTTCTCCCTCCCGCAAAACCAAGAGACCTCATGATCTC 123
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QY 184 GTTCAACTGTGACGTGAGCGGCTGTGAGGTGCAATATGCCAAGCAAAAGCCGCGGAGGA 243
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QY 244 GCAGTCAACAGACGTAACCGGCTGTGACGCTCTCAACGCTCTGCAACAGACCTGAGCT 303
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QY 604 GAGCAGGTGGACAGAGGGGAAAGCTCTTCTCAATGCTCCGATGATGATGAGGCTTGCACA 663
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RESULT 14
AR031186 1428 bp DNA linear PAT 29-SEP-1999
LOCUS AR031186
DEFINITION Sequence 19 from patent US 5866125.
ACCESSION AR031186
VERSION AR031186.1 GI:5945475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1428)
AUTHORS Brans, P., Chamel, S., Salim, P., Pan, L.-Z., Walsh, E.E., Heard, C., Janne, and Newman, R. Anthony.
TITLE Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof
JOURNAL Patent: US 5866125-A 19 02-FEB-1999;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .1428
/organism="unknown"
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ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1428;
Best Local Similarity 99.9%; Pred. No. 2.3e-125;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGGCCAGCCTGAACT 63
Db 726 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGGCCAGCCTGAACT 785
QY 64 CTTGGGGGAGCCGTAGCTTCTTCTCCCAAAACCCAGAGACCTCTATGATCTC 123
Db 786 CTTGGGGGAGCCGTAGCTTCTTCTCCCAAAACCCAGAGACCTCTATGATCTC 845
QY 124 CCGACCCCTGAGGTCAATGCGGTGTGTGACGTGAGCCAGAAACCTTGAAGTCAA 183
Db 846 CCGACCCCTGAGGTCAATGCGGTGTGTGACGTGAGCCAGAAACCTTGAAGTCAA 905
QY 184 GTTCAACTGTGACGTGACGGCGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 243
Db 906 GTTCAACTGTGACGTGACGGCGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 965
QY 244 GCACTACAAAGACGTAACCGGTGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 303
Db 966 GCACTACAAAGACGTAACCGGTGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 1025
QY 304 GAAATGCAAGAGTACAGTGAAGTCTTCAACAAAGCCTTCCAGCCCATTCAGAA 1085
Db 1026 GAAATGCAAGAGTACAGTGAAGTCTTCAACAAAGCCTTCCAGCCCATTCAGAA 1085
QY 364 AACCATCTCCAAAGCCAAAGGAGCCCGGAAACCAAGGTGACACCTTGCCTCCATC 423
Db 1086 AACCATCTCCAAAGCCAAAGGAGCCCGGAAACCAAGGTGACACCTTGCCTCCATC 1145
QY 424 CCGGATGAGTGAACCAAGGACAGTCACTGCTGCTTCAAGAGCTTCTATCC 483
Db 1146 CCGGATGAGTGAACCAAGGACAGTCACTGCTGCTTCAAGAGCTTCTATCC 1205
QY 484 CAGCAGATTCGCCGTGAGTGGAGAGCAATGGGACGCCGGAACAACTACAAAGCCAC 543

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RESULT 15
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LOCUS AR042591
DEFINITION Sequence 19 from patent US 5811524.
ACCESSION AR042591
VERSION AR042591.1 GI:5963087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1428)
AUTHORS Brans, P., Chamel, S., Salim, P., Pan, L.-Z., Walsh, E.E., Heard, C., Janne, and Newman, R. Anthony.
TITLE Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof
JOURNAL Patent: US 5811524-A 19 22-SEP-1998;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .1428
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ORIGIN

Query Match 90.4%; Score 694.4; DB 6; Length 1428;
Best Local Similarity 99.9%; Pred. No. 2.3e-125;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGGCCAGCCTGAACT 63
Db 726 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTGGCCAGCCTGAACT 785
QY 64 CTTGGGGGAGCCGTAGCTTCTTCTCCCAAAACCCAGAGACCTCTATGATCTC 123
Db 786 CTTGGGGGAGCCGTAGCTTCTTCTCCCAAAACCCAGAGACCTCTATGATCTC 845
QY 124 CCGACCCCTGAGGTCAATGCGGTGTGTGACGTGAGCCAGAAACCTTGAAGTCAA 183
Db 846 CCGACCCCTGAGGTCAATGCGGTGTGTGACGTGAGCCAGAAACCTTGAAGTCAA 905
QY 184 GTTCAACTGTGACGTGACGGCGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 243
Db 906 GTTCAACTGTGACGTGACGGCGTGTGACGTGACGTGACGTGACGTGACGTGACGTGAC 965
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Search completed: March 8, 2005, 08:08:09
 Job time : 3398 secs

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